Marine Life Protection Act Initiative



MPA Spacing Work Group Progress Report

Presentation to the MLPA Master Plan Science Advisory Team Joint Meeting for the South Coast and North Coast Study Regions October 30, 2009 • Eureka, California

Dr. Will White, Master Plan Science Advisory Team



MPA Spacing Guideline

- Marine Protected Area (MPA) Spacing Guideline
 - MPAs should be located within 31-62 miles of each other
- Guideline is a Proxy for Larval Connectivity in an MPA Network
 - Addresses Marine Life Protection Act goal #6
- Cons
 - Fixed threshold
 - Proxy, not a direct evaluation of connectivity
 - Assumes spatially homogeneous connectivity
- Pros
 - Simplicity, ease of use
 - Works well if connectivity is spatially homogeneous
 - Good for getting started with MPA design process

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Bioeconomic Modeling

• Bio-economic models incorporate:

- Life history characteristics of model species
- Adult home range size
- Larval dispersal based on ocean circulation model
- Bio-economic models:
 - Directly evaluate population persistence
 - Do not represent genetic connectivity
- How can the SAT evaluate connectivity across the study region and gaps in connectivity between adjacent MPAs?



A New Metric of Connectivity

A new connectivity metric should:

- Build upon existing bio-economic models
- Measure the rate of genetic transmission across the network (e.g. movement of a neutral allele across the coastline)
- Reveal "gaps" between proposed MPAs
- Provide useful information for MPA design
- A connectivity metric would only be used to evaluate proposed MPA networks
 - MPA spacing guidelines (31-62 miles) are useful guidance for MPA design



Possible Connectivity Metrics

- Several Options Considered by SAT MPA **Spacing Work Group**
 - All involve extending bioeconomic models to include a population genetics component
 - Movement of a neutral allele among model cells at equilibrium
 - Details still being discussed within work group



Possible Connectivity Metrics

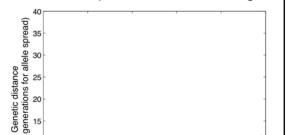
- Options Considered
 - A) Neutral allele model with finite population size
 - Stochastic, with genetic drift
 - Average over multiple simulations
 - B) Neutral allele model with infinite population size
 - Non-stochastic
 - C) Markov chain model
 - Not fully developed yet, but intended to be shortcut approximation to either A or B



Example Preliminary Results: Option A

(Number of

- Population on linear coastline, diffusive larval dispersal
- Single haploid locus
- All patches homozygous for allele A, one patch homozygous for allele B instead
- How fast does B spread to other patches?
- Each point = 1 pair of patches



Example: Without fishing

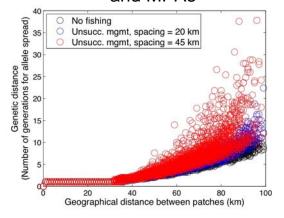
Genetic distance increases with geographic distance.

20 40 60 Distance between patches (km)

Example Preliminary Results: Option A

- Population on linear coastline, diffusive larval dispersal
- Single haploid locus
- All patches homozygous for allele A, one patch homozygous for allele B instead
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Example: With fishing and MPAs

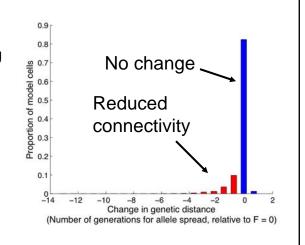


Fishing increases genetic distance.



Example Preliminary Results: Option A

- Measure change in genetic distance versus without fishing
- Overall metric
 - Mean reduction in connectivity
 - Mean end-to-end connectivity
- Which MPA pairs exhibit reduced connectivity? (relative to example without fishing)





Current Status

• Genetic model still in early development

- Determining needed level of sophistication
- Identifying key parameters (e.g., population size)
- Exploring how to translate MPA-specific results into useful advice for adjusting proposed MPA networks



Current Status

• Is a connectivity metric necessary?

- Genetic model potentially adds information
- Genetic model is more complicated and less intuitive than the spacing guideline
- With spatially homogenous larval transport, existing spacing guideline could serve as a proxy for connectivity
- If there are discontinuities in larval dispersal in the north coast study region, then a connectivity metric may be useful for evaluating gaps between proposed MPAs in a network